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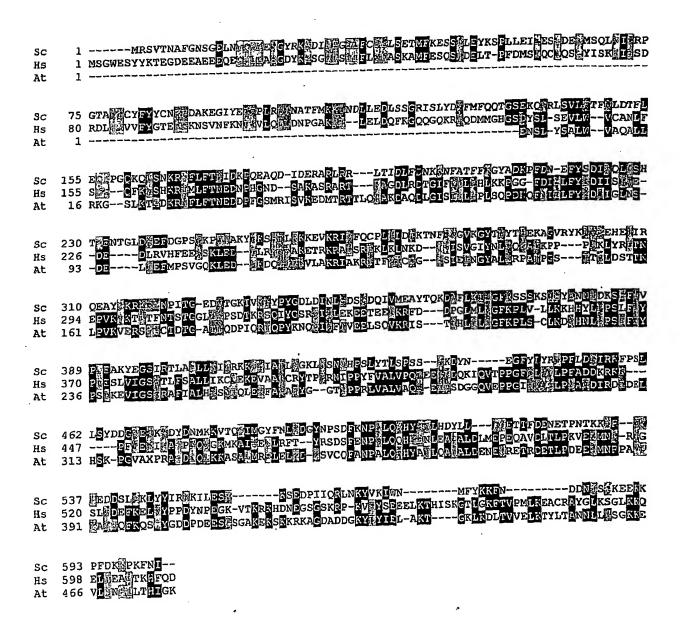
Fig. 1

| Strain | LB' T-DNA RB' CAGGATATATTCAATTGTAAAT-CTCCGA-GG (| Chromosome, coordinate and location |
|-----------|---|---|
| WT.51 | -4 5'ATTGTATTATATATTCAATTGTAAAT-CTCCGA-GGTA 3' | XIV, 185311 (1 bp of target site DNA deleted), int. region |
| rad50k.1 | 5TGTGGGTGTGATATTCAATTGTAAAT-CTC—CGA-GG 3' | XV, 1091277, tel. region |
| rad50k.5 | 5' GGGGGCATCAGTATTCAATTGTAAAT-CTCCGA-GG 3' | XII, 465986, rDNA region |
| rad 50k.6 | 5' GAGGTAGATGTGAGAGAGTGTGTGTGGGTGTGAAGTCGA 3' | XV, 1091276, tel. region |
| | -3 | |
| mre11k.4 | 5' TCTGGTAGATATATTCAATTGTAAAT-CTCCGA-GG 3' | XII, 459692/468829, rDNA region |
| mre11k.5 | 5' CACATATTTCTCATTCAATTGTAAAT-CTCCGA-GG 3' | VII/X/XIII, 536090 OR 541678/ 472487 OR 483659/196667, LTR |
| mre11k.8 | 5' CGACTACTTTATATCCAATTGTAAAT-CTCCGA-GG 3' | XIV, 6060, subtel. region |
| mre11k.11 | 5' GAAGAACCCATTATTCAATTGTAAAT-CTCCGA-GG 3' | XIV, 4866, subtel. region |
| mre11k.14 | 5' TGGGTGTGGGTTATTCAATTGTAAAT-CTCCGA-GG 3' | VIII, 562588, tel. region |
| mre11k.17 | 5' TGGGTGTGTGTTCAATTGTAAAT-CTCCGA-GG 3' | XII, 5727, subtel. region |
| | -10 | |
| xrs2k.1 | 5' TGTGTGGGTGTGGGTCAATTGTAAAT-CTCCGA-GG 3' | IX/X, 69/52, tel. region |
| xrs2k.17 | 5' CGTCAAGGATATATTCAATTGTAAAT-CTCCGA-GG 3' | XII, 1071797, subtel. region |

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Fig. 2

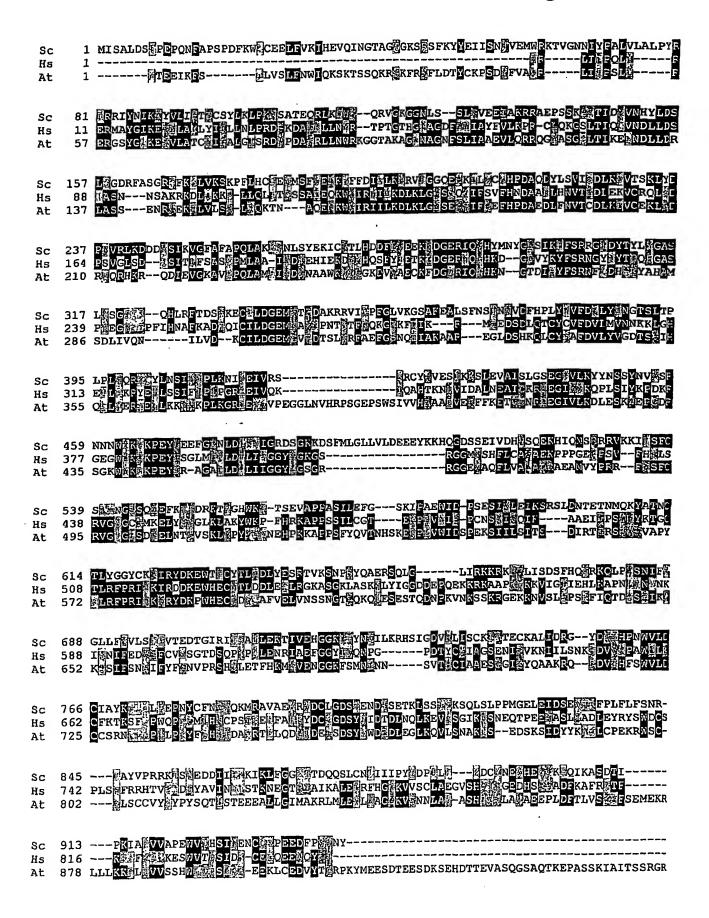


TITLE: NUCLEIC-ACID INTERGRATION IN EUKARYOTES

Inventor: Hooykaas et al. Docket No.: 2183-6028US

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Fig. 3A



TITLE: NUCLEIC ACID INTERGRATION IN EUKARYOTES Inventor: Hooykaas et al. Docket No.: 2183-6028US

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Fig. 3B

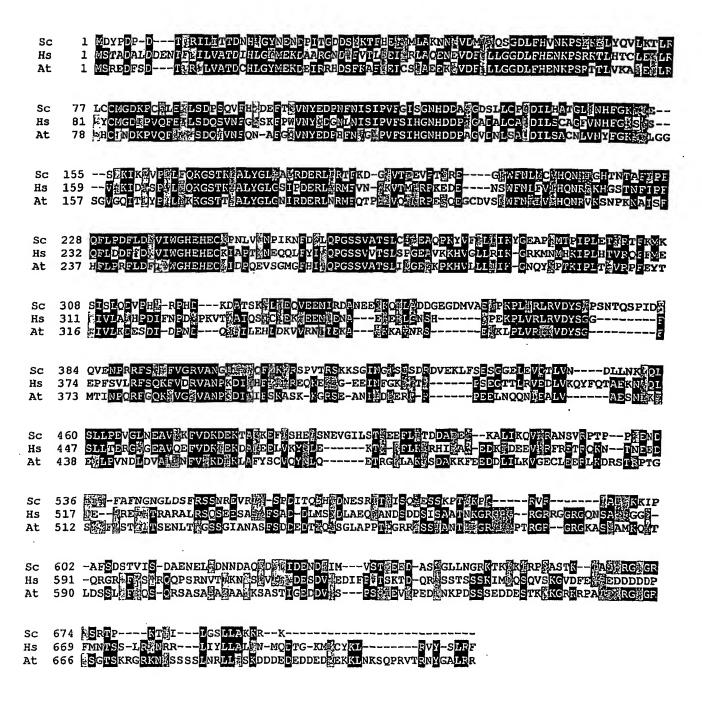
| Sc | | |
|----|------|--|
| At | 957 | |
| Sc | | |
| Нs | | |
| At | 1037 | QTQRVQRSRRGKKAAKIGGDESDENDELDGNNNVSADAEEGNAAGRSVENEETREPDIAKYTESQQRDNTVAVEEALQDS |
| Sc | | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |
| Hs | | |
| At | 1117 | ${\tt RNAKTEMDMKEKLQIHEDPLQANLMKMFPIPSQKTTETSNRTTGEYRKANVSGECESSEKRKLDAETDNTSVNAGAESDV}$ |
| SC | | |
| ls | | |
| ٩t | 1197 | VPPLVKKKKVSYRDVAGELLKDW |

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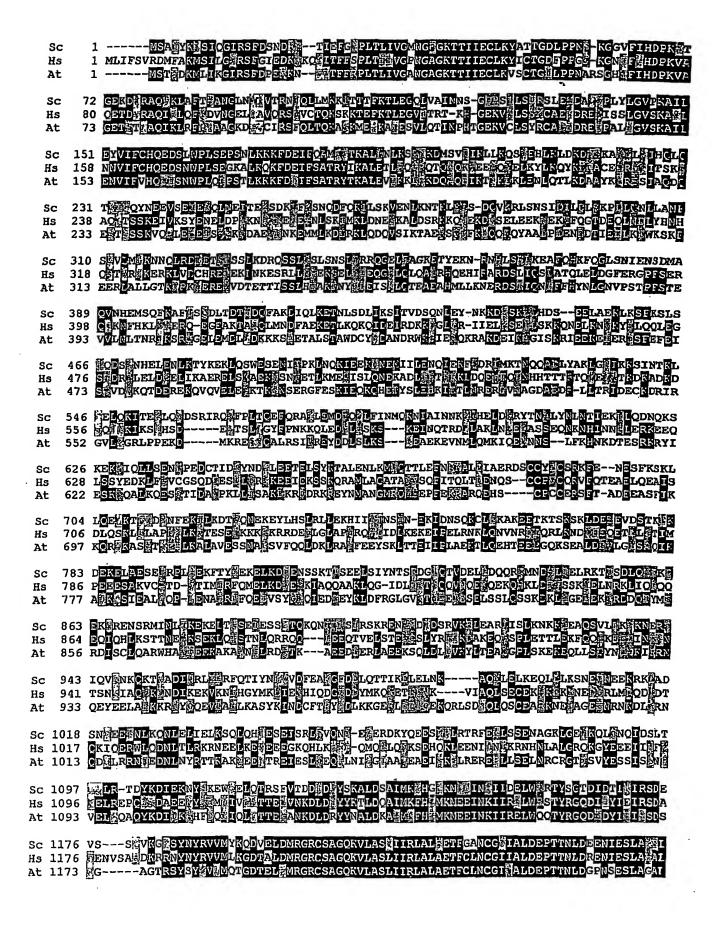
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Fig. 4



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Fig. 5



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Fig. 6

| • | | 1 50 |
|-----------------|----------------|--|
| At | (1) | |
| Hs | (1) |)MERKI SR |
| Sc | (1) | |
| Consensus | (1) | IETL E SKIS |
| | | |
| | | 51 100 |
| At | (28) | LRLEISGADPIFVKGTWHNSRFDISVTDGSSS |
| Hs | (8) | THLVSEPSITHETOVSWEKTLESCHVITTTOGHSA |
| Sc Consensus | (51) | EKMLYSEGTGITSKSSTGINDLRIFTGENIDEESKKYVWYELLKMLTGHK IKLLIS A IFLK SW S F ISLTDG SA |
| Consensus | (31) | INDUIS A IEBN SW S E ISBIDG SA |
| | | 101 150 |
| At | (60) | Wicnatereväeraaqwoopvseyl-klaeqyigfq |
| Hs | (43) | WTGTVSESEISQEADDMAMEKGKYVGELRKALLSGA |
| Sc | (101) | VYIASLDEKVVFTKWTCRMODDEVWKVVMELESSAITRKTAELTTHPV |
| Consensus | (101) | WTC MSEDEVA A DLD S YI KLAE L |
| | | |
| At | /0E\ | 151 200 |
| AC Hs | (95) | OPNSVYSFSDALEGSKRĪSWTFEKEGĪKLEWRWKCKPSDDSKKLTVGLLD GPADVYTFNFSKESCYFFFEKNLKDVSFRLGSFNLEKVĒNPAEVIRELIC |
| Sc | (149) | KKGEIDLFEMADKLYKDICCVNDSYRNIKESDSSNRNRVEQLARERELLD |
| Consensus | | PADVYSF A E K I NDKD S KE F K DD I RELLD |
| | (===, | The state of the s |
| | | 201 250 |
| At | (145) | FLMEANIRLSEEVYNKTR-SFEKMRSEAERCLAQGEKLCDEKTEFESATY |
| Hs | | YCLDTIAENQAKNEHLOK-ENERLIRDWNDVQGRFEKCVSAKHALEUDLY |
| Sc | (199) | KLLETRDERTRAMMVTLLNEKKKKTRELHETLRONNIKLSDDDVLDSALI |
| Consensus | (201) | FLLET E S MM K E EKLIRE DILAQ EK LSDKD LESALY |
| | | 251 300 |
| At | (194) | AKFLSVLNAKKAKURALRDKEDSVRVVEE |
| Hs | (178) | KRFILVLNEKKTKIRSLHNKLLNAAQEREKDIKQEGE |
| Sc | (249) | NTEVOKPI SEL NSPGKEMEREKTVVEPONLOKKLKDTSRRRANRKI SNOS |
| Consensus | (251) | KFISVLNA KK KIR AL KL A RE |
| | | |
| | | 350 |
| At | (223) | |
| Hs Sc | (512) | TAICSEMTADROPVYDESTDEESENOTOLISGLASAAVSKODSIISSLDVIT VIKMEDDDFDDFGFFGLSKRPIITAKDKLSEKYDDITSFGDDTQSISFES |
| Consensus | (301) | Mu |
| COMBCMBUS | (301) | EDS DK FD SK DD A DDLS KASAA SKGD S S S |
| | | 351 400 |
| At | (265) | ••• |
| Hs | (265) | DIAPSRKRRQRMQRNLGTEPKMAPQENQLQEKEKPDSSLPETSKKEHISA |
| Sc | (349) | DSSSDVQKHLVSLEDNGIQISAGRSDEDYGDISGSESETDASAGEKKSSN |
| Consensus | (351) | DAK GAD D DS SAS |
| | | |
| | | 401 423 |
| | (265) | |
| | | ENMSLETLRNSSPEDLFDEI |
| | (399) (401) | HSEQSGNDREPCLQTESETDIET |
| Consensus | (401) | R D |